SEQUENCE LISTING

<110> Eberhard Hildt, Prof. Hofschneider

<120> Particles for Gene Therapy

<130> 319-2 US

<140> PCT/DE00/00363

<141> 2000-02-04

<150> DE 199 04 800.2

<151> 1999-02-05

<160> 19

<170> PatentIn Ver. 2.1

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<211> 347

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:

Fusion protein comprising a LHBs and heterologous binding site RGD

<400> 1

Met Gly Arg Gly Asp Gly Ala Gly Ala Phe Gly Leu Gly Phe Thr Pro

1 5 10 15

Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu

Glu Thr Leu Pro Ala Asn Pro Pro Pro Ala Ser Thr Asn Arg Gln Ser 35 40 45

Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu Arg Asn Thr His Pro 50 55 60

Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Thr Leu Gln Asp 65 70 75 80

Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly 85 90 95

Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe 100 105 110

Ser Arg Ile Gly Asp Pro Ala Leu Asn Met Glu Asn Ile Thr Ser Gly
115 120 125

Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr

Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu 145 150 155 160

Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly Gln Asn Ser Gln Ser 165 170 175

Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Thr Cys Pro Gly
180 185 190

Tyr Arg Trp Met Cys Leu Arg Arg Phe IIe IIe Phe Leu Phe IIe Leu 195 200 205

Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met 210 215 220

Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr Ser Thr Gly 225 230 235 240

Pro Cys Arg Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser Met Tyr Pro 245 250 255

Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro 260 265 270

Ile Pro Ser Ser Trp Ala Phe Gly Lys Phe Leu Trp Glu Trp Ala Ser 275 280 285

Ala Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe 290 295 300

Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp 305 310 315 320

Tyr Trp Gly Pro Ser Leu Tyr Ser Ile Leu Ser Pro Phe Leu Pro Leu 325 330 335

Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile 340 345

<210> 2

<211> 215

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:

Fusion protein comprising a HBcAg, a cell-permeability-mediating polypeptide and heterologous binding site RGD

<400> 2

Met Pro Leu Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro Thr Val Gln
1 5 10 15

- Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile Asp Pro 20 25 30
- Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser 35 40 45
- Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu 50 55 60
- Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr 65 70 75 80
- Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala 85 90 95
- Thr Trp Val Gly Val Asn Leu Glu Asp Pro Glu Phe Arg Gly Asp Ala 100 105 110
- Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys 115 120 125
- Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg 130 135 140
- Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr 145 150 155 160
- Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro 165 170 175
- Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Thr 180 185 190
- Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser 195 200 205
- Gln Ser Arg Glu Pro Gln Cys 210 215
- <210> 3
- <211>663
- <212> DNA
- <213> Artificial sequence
- <220>
- <223> Description of the artificial sequence:

DNA coding for a fusion protein comprising a HBcAg, a cell-permeability-mediating polypeptide and heterologous binding site RGD

<400> 3

atgcccatat cgtcaatctt ctcgaggatt ggggaccctg gatccactac tgttcaagcc

120 tecaagetgt geettgggtg getttgggge atggacateg accettataa agaatttgga getactgtgg agttactete gtttttgeet tetgaettet tteetteagt acgagatett 240 ctagataccg ceteagetet gtategggaa geettagagt eteetgagea ttgtteacet caccatactg cactcaggea ageaattett tgctgggggg aactaatgac tctagctacc 300 360 tgggtgggtg ttaatttgga agatccagaa ttccgaggcg acgcgtctag agacctagta 420 gtcagttatg tcaacactaa tatgggccta aagttcaggc aactcttgtg gtttcacatt 480 tettgtetea ettttggaag agaaacegtt atagagtatt tggtgtettt eggagtgtgg attegeacte etecagetta tagaceacea aatgeeecta teetateaae aetteeggaa 540 600 actactgttg ttagacgacg aggcaggtcc cctagaagaa gaactccctc gcctcgcaga cgaaggtete aategeegeg tegeagaaga teteaatete gggaacetea atgitagtat 660 663 tcc

<210> 4 <211> 1047 <212> DNA <213> Artificial sequence

<220>

<223> Description of the artificial sequence:

DNA coding for a fusion protein comprising a LHBs and heterologous binding site RGD

<400>4

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tatcaaggta tgttgcccgt ttgtcctcta attccaggat ceteaaceae cagcacggga	720
ccatgcegaa cetgcatgae tactgeteaa ggaaceteta tgtatecete etgttgetgt	780
accaaacctt cggacggaaa ttgcacctgt attcccatcc catcatcctg ggctttcgga	840
aaatteetat gggagtggge eteageeegt tteteetgge teagtttaet agtgeeattt	900
gttcagtggt tcgtagggct ttcccccact gtttggcttt cagttatatg gatgatgtgg	960
tattgggggc caagtetgta cagcatettg agteeetttt taeegetgtt accaatttte	1020
ttttgtcttt gggtatacat ttaaacc 1047	

<210> 5 <211> 35 <212> DNA <213> Artificial sequence <220>

<223> Description of the artificial sequence:
Primer

<400> 5

ccatattett gggaacaaga tatecageae gggge

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<210> 6
<211> 33
<212> DNA
<213> Artificial sequence
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<223> Description of the artificial sequence:
Primer

<400> 6

ggattgctgg tggaagatat ctgccccgtg ctg

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<210> 7 <211> 33 <212> DNA <213> Artificial sequence <220>

<223> Description of the artificial sequence: Primer	
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<400> 8	
gccccgtgct ggatateate ttgttcccaa gaatatgg	38
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aaaagatctg gccgtggcga aggagctgga gcattc	36
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<400> 10	
aaaagatctg gtttaaatgt atacccaaag	30
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	<212> DNA <213> Artificial sequence		
	<220> <223> Description of the artificial sequence: Primer		
	<400> 11		
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	<210> 12 <211> 30 <212> DNA <213> Artificial sequence		
	<220> <223> Description of the artificial sequence: Primer		
	<400> 12		
	ggggatateg gtegatgtee atgeeceaaa		30
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nnnggateca etgtteaage eteeaagetg	30
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<220> <223> Description of the artificial sequence: Primer	,
<400> 17	
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<210> 18 <211> 39 <212> DNA <213> Artificial sequence	
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<400> 18	

nnngaattee gaggegaege gtetagagae etagtagte

39

20